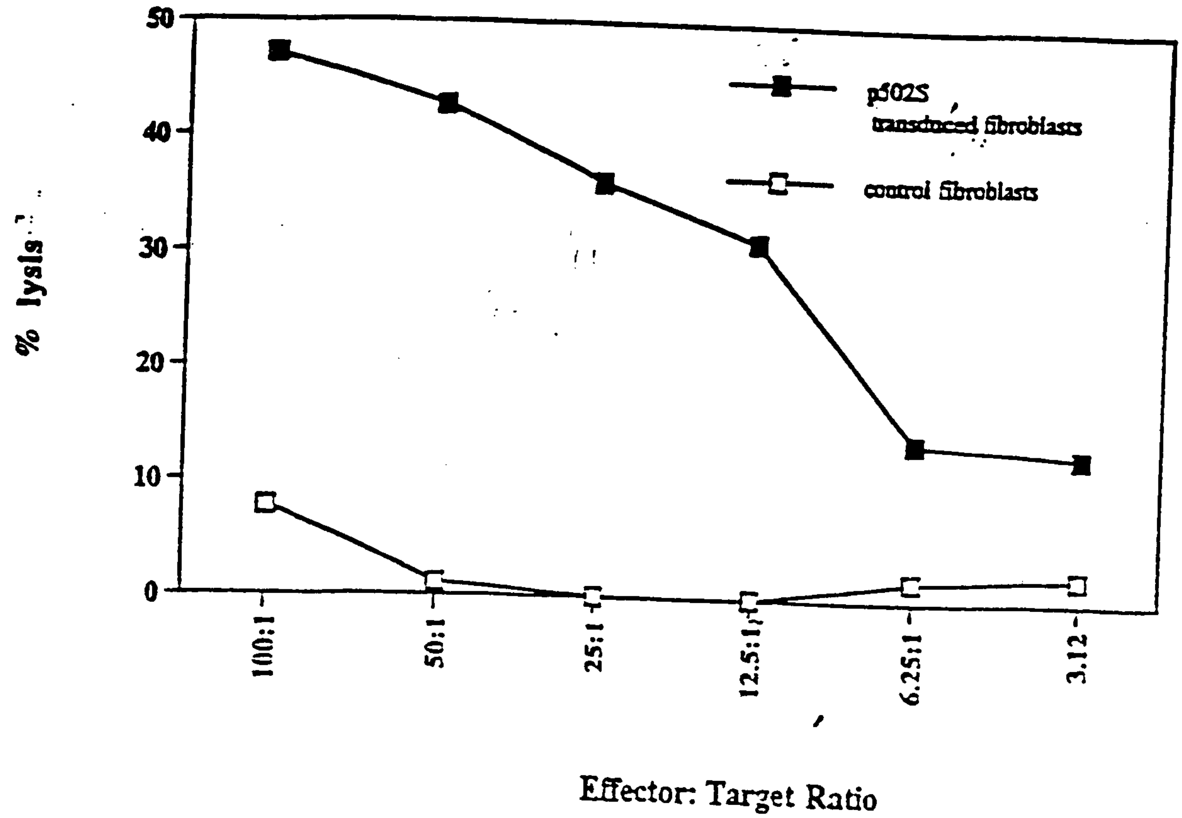

% lysis
50
40
30
20
10
0
p502S transduced fibroblasts
control fibroblasts
100:1
50:1
25:1
12.5:1
6.25:1
3.12
Effector: Target Ratio

FIG. 1

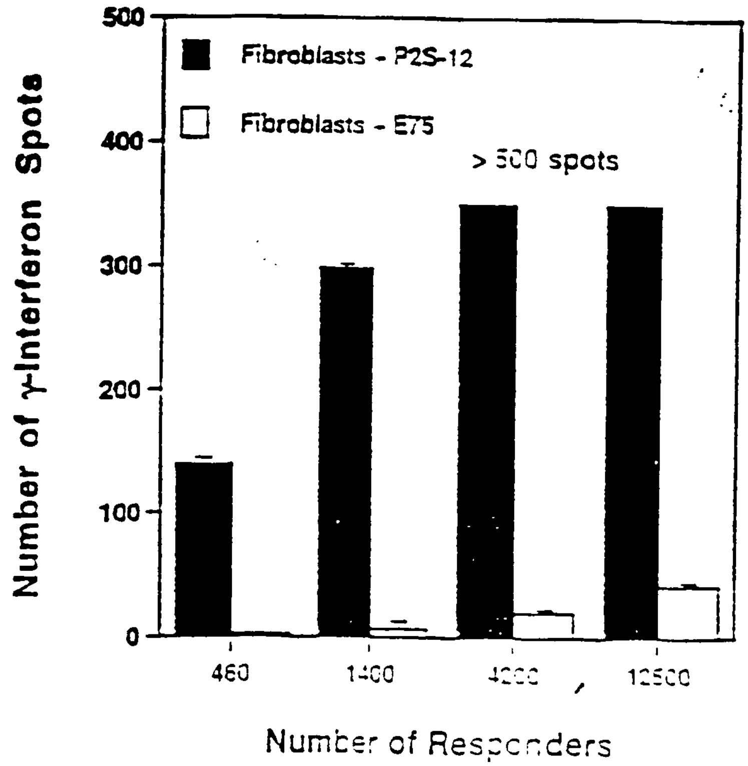
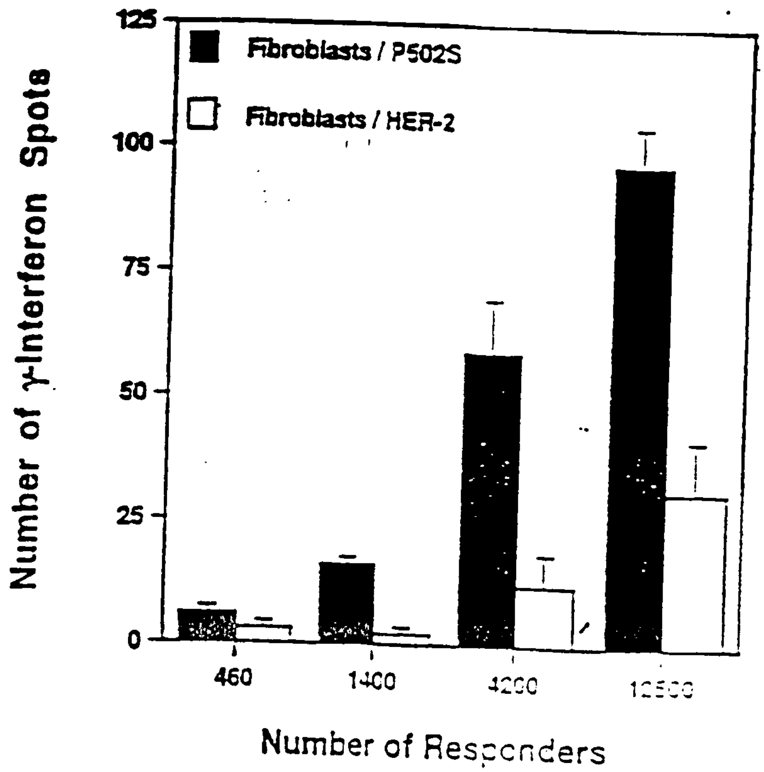
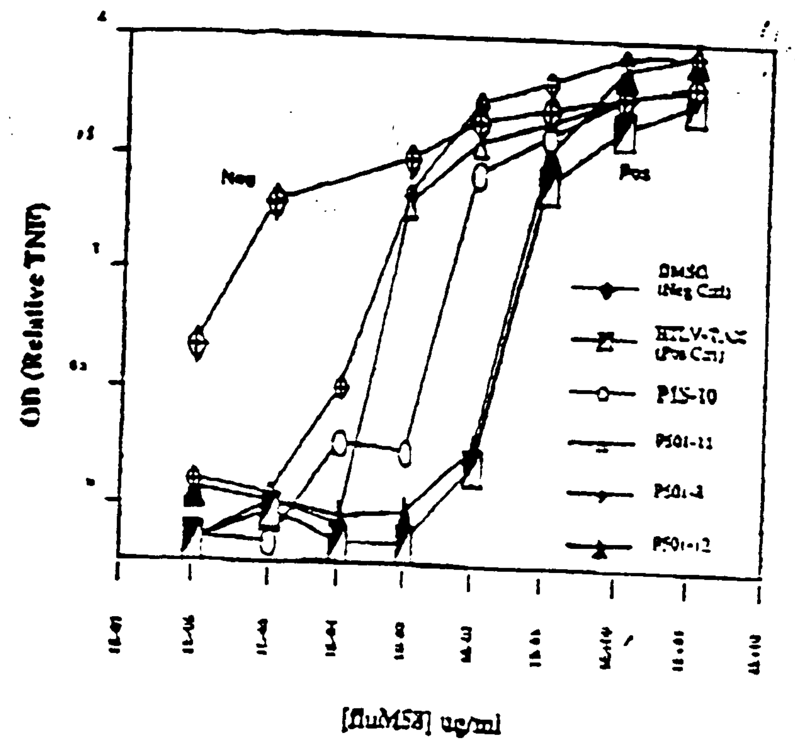

Fibroblasts - P2S-12
Fibroblasts - E75
> 500 spots
Number of γ-Interferon Spots
0
100
200
300
400
500
460
1400
12500
Number of Responders

FIG. 2A



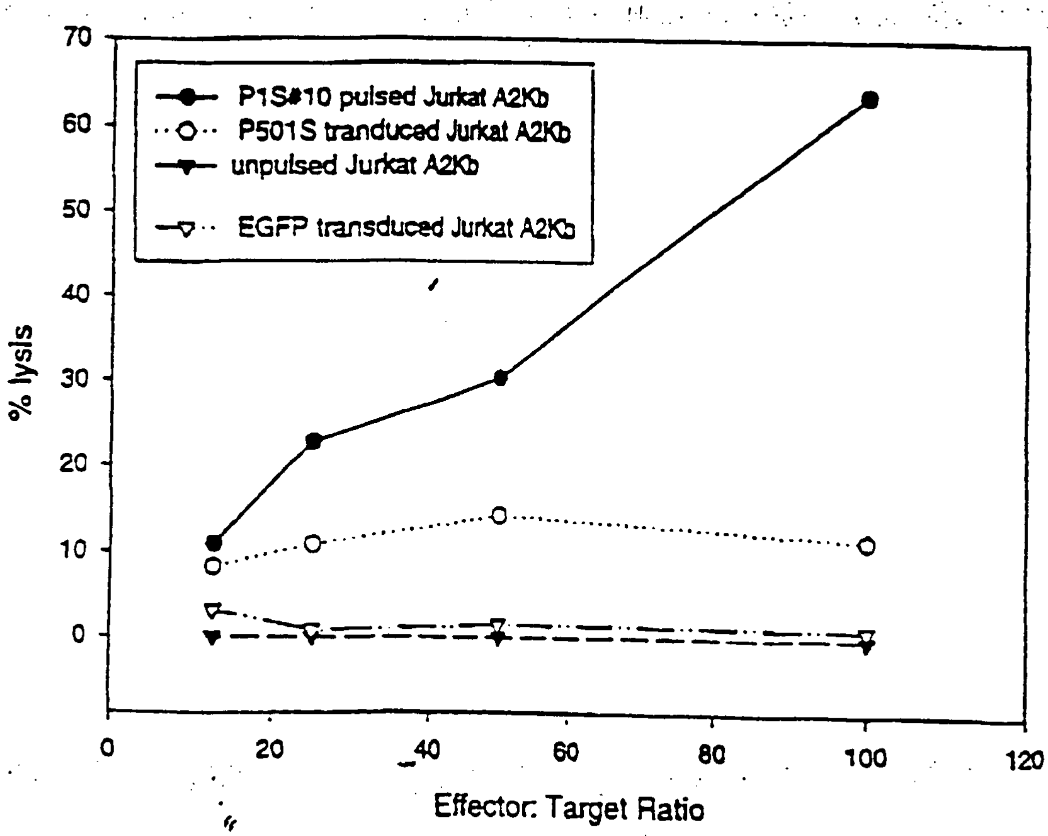
Fibroblasts / P502S
Fibroblasts / HER-2
Number of γ-Interferon Spots
125
100
75
50
25
0
460
1400
Number of Responders

FIG. 2B



OD (Relative TNF)
Neg
Pos
DMSO (Neg Ctrl)
(Pos Ctrl)
P1S-10
P501-11
P501-4
P501-12
[fluMS8] ug/ml

Figure 3



P1S#10 pulsed Jurkat A2Kb
P501S tranduced Jurkat A2Kb
unpulsed Jurkat A2Kb
EGFP transduced Jurkat A2Kb
% lysis
Effector: Target Ratio
70
60
50
40
30
20
10
0
0
20
40
60
80
100
120

Figure 4

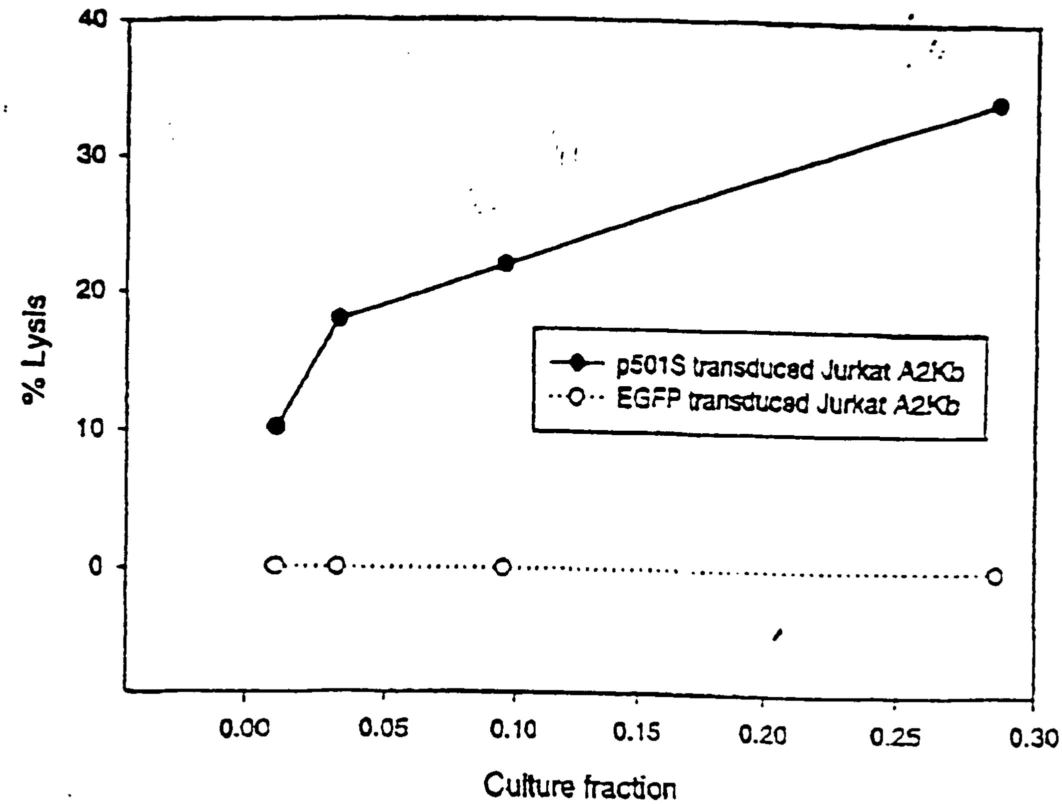
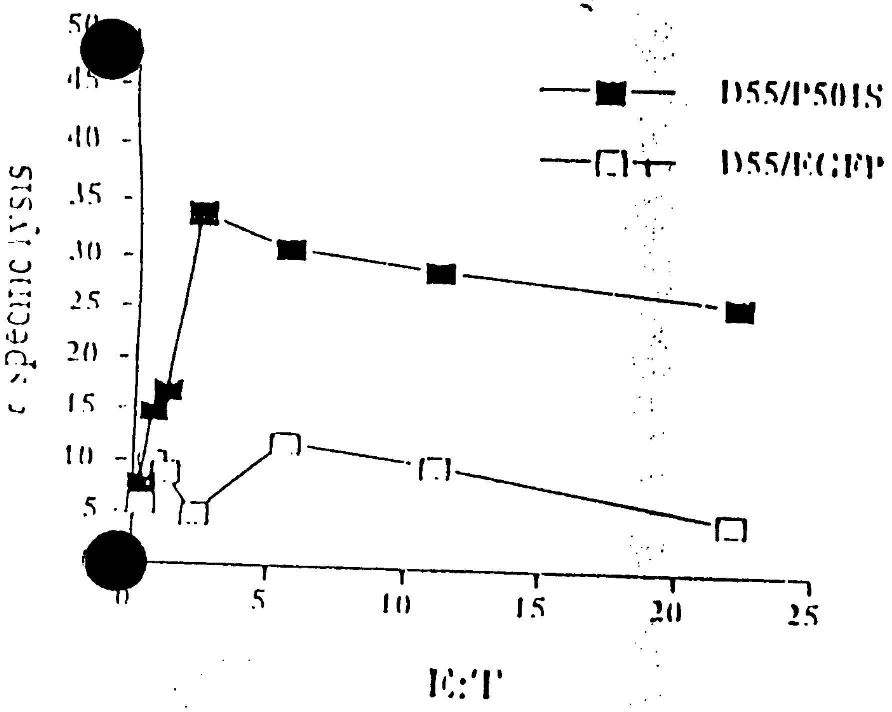
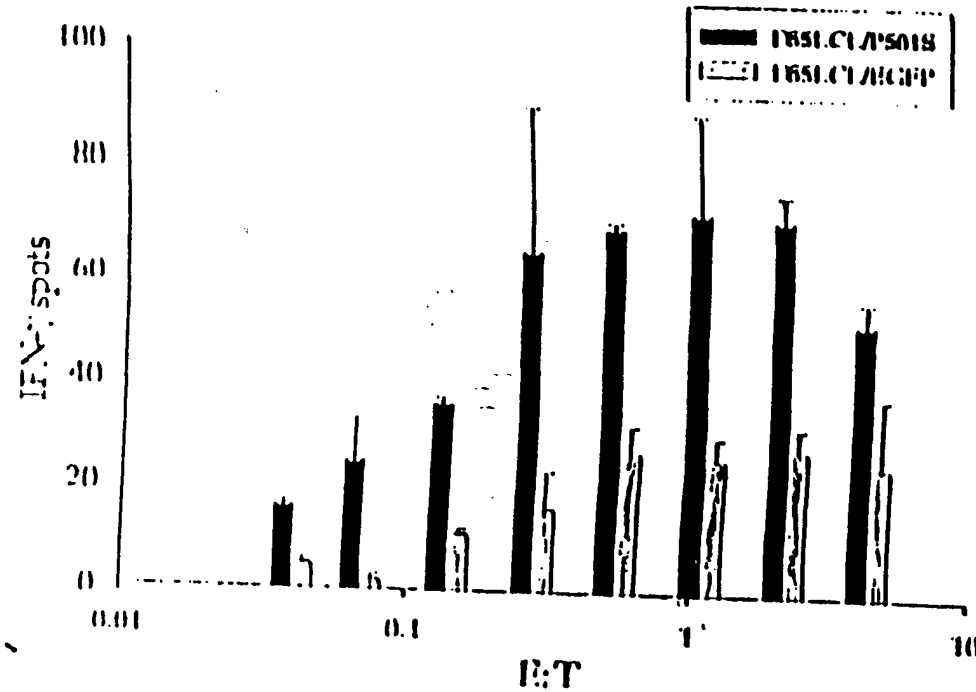

40
30
20
10
0
% Lysis
0.00
0.05
0.10
0.15
0.20
0.25
0.30
Culture fraction
p501S transduced Jurkat A2Kb
EGFP transduced Jurkat A2Kb

Figure 5



% specific lysis
D55/P501S
D55/EGFP
E:T

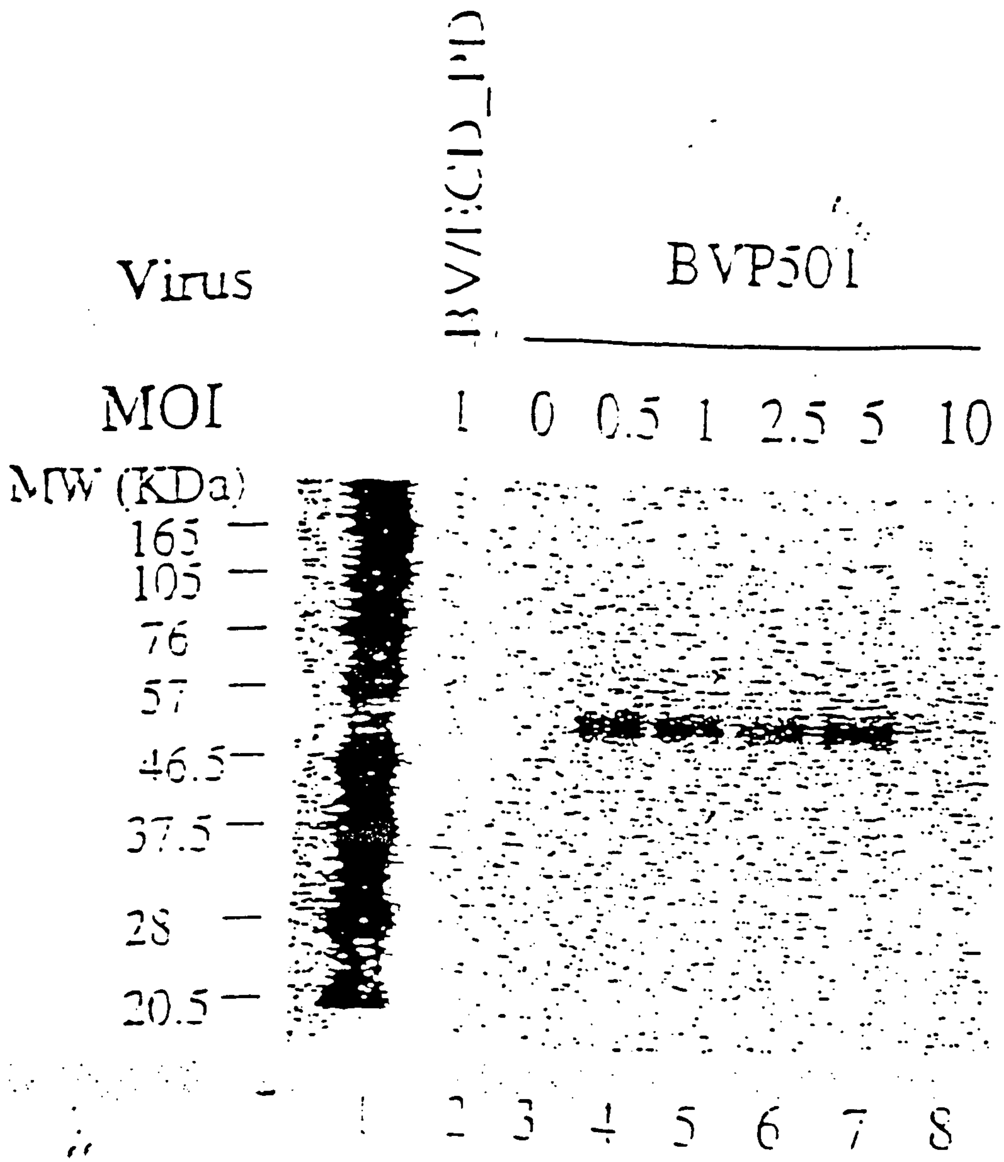
Fig. 6A



D55I.Cl/P501S
D55I.Cl/EGFP
IFN-γ spots
E:T

Fig. 6B

E[illegible]pression of P501S
by the B[illegible]virus Expression System



0.6 million high [illegible] 6-well plate were infected with an unrelated control virus BV/ECD_PD [illegible] without virus (lane 3) or with recombinant baculovirus for P501 at differ[illegible] (lane 4 - 8). Cell lysates were run on SDS-PAGE under the reducing [illegible] and analyzed by Western blot with a monoclonal antibody against [illegible] P501S-10E3-G4-D3). Lane 1 is the biotinylated protein molecular weight ma[illegible] (Lab).

Fig. 7

Figure 8. Mapping of the epitope recognized by 10E3-G4-D3

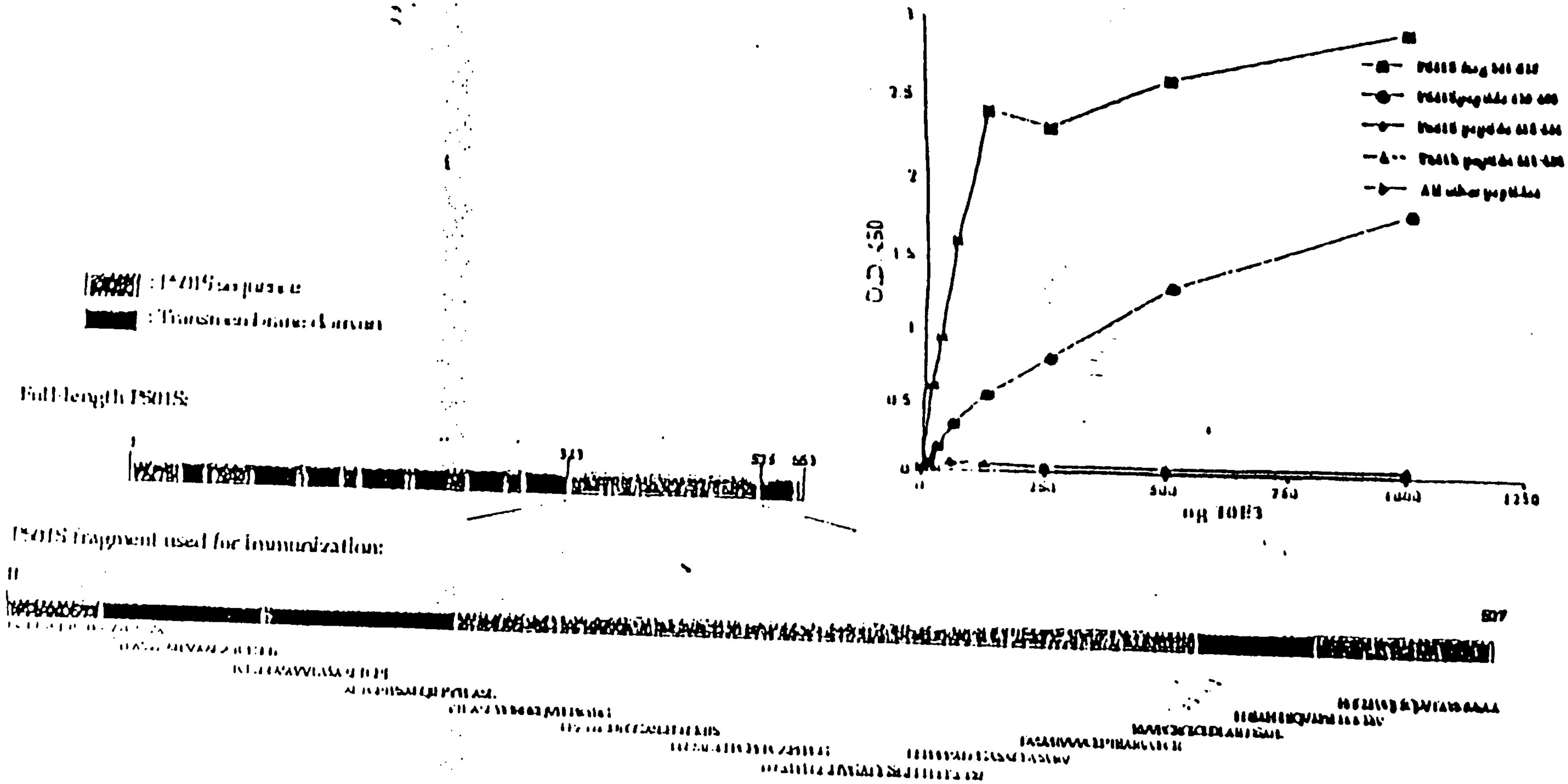


Fig 8

7

Figure 1. Schematic of P501S with predicted transmembrane, cytoplasmic, and extracellular regions

MVQRLWVSRLLRHRK AQLLLVNLLTFGLEVCLAAGIT **YVPPLLLEVGVEEKFM** TMVLGIGPVLGLVCVPLLGSAS

DHWRGRYGRRRP FIWALSLGILLSLFLIPRAGWL **AGLLCPDPRPLE** LALLILGVGLLDFCGQVCFTPL

EALLSDLFRDPDHCRQ AYSVYAFMISLGGCLGYLLPAI **DWDTSALAPYLGTQEE**

CLFGLLTLIFLTCVAATLLV *AEEAALGPTEPAEGLSAPSLSPHCCPCRARLAFRNLGALLPRL*

HQLCCRMPRTLRR LFVAELCSWMALMTFTLFYTDF **VGEGLYQGVPRAEPGTEARRHYDEGVR**

MGSLGLFLQCAISLVFSLVM *DRLVQRFGTRAVYLAS* VAAFPVAAGATCLSHSVAVVTA **SAA**

LTGFTFSALQILPYTLASLY *HREKQVFLPKYRGDTGGASSEDSLMTSFLPGPKPGAPFPNGHVGAGGSGL*

LPPPPALCGASACDVSVRVVVGEPTEARVVPGRG ICLDLAILDSAFLLSQVAPSLF **MGSIVQLSQS**

VTAYMVSAAGLGLVAIYFAT *QVVFDKSDLAKYSA*

Underlined sequence: Predicted transmembrane domain; **Bold sequence: Predicted extracellular domain;** *Italic sequence:* Predicted intracellular domain. Sequence in bold/underlined: **used to generate polyclonal rabbit serum**

Localization of domains predicted using HMMTOP (G.E. Tusnady and I. Simon (1998) **Principles** Governing Amino Acid Composition of Integral Membrane Proteins: Applications to topology **Prediction.J.Mol Biol. 283,** 489-506.

Fig. 9

Genomic Map of (5) Corixa Candidate Genes

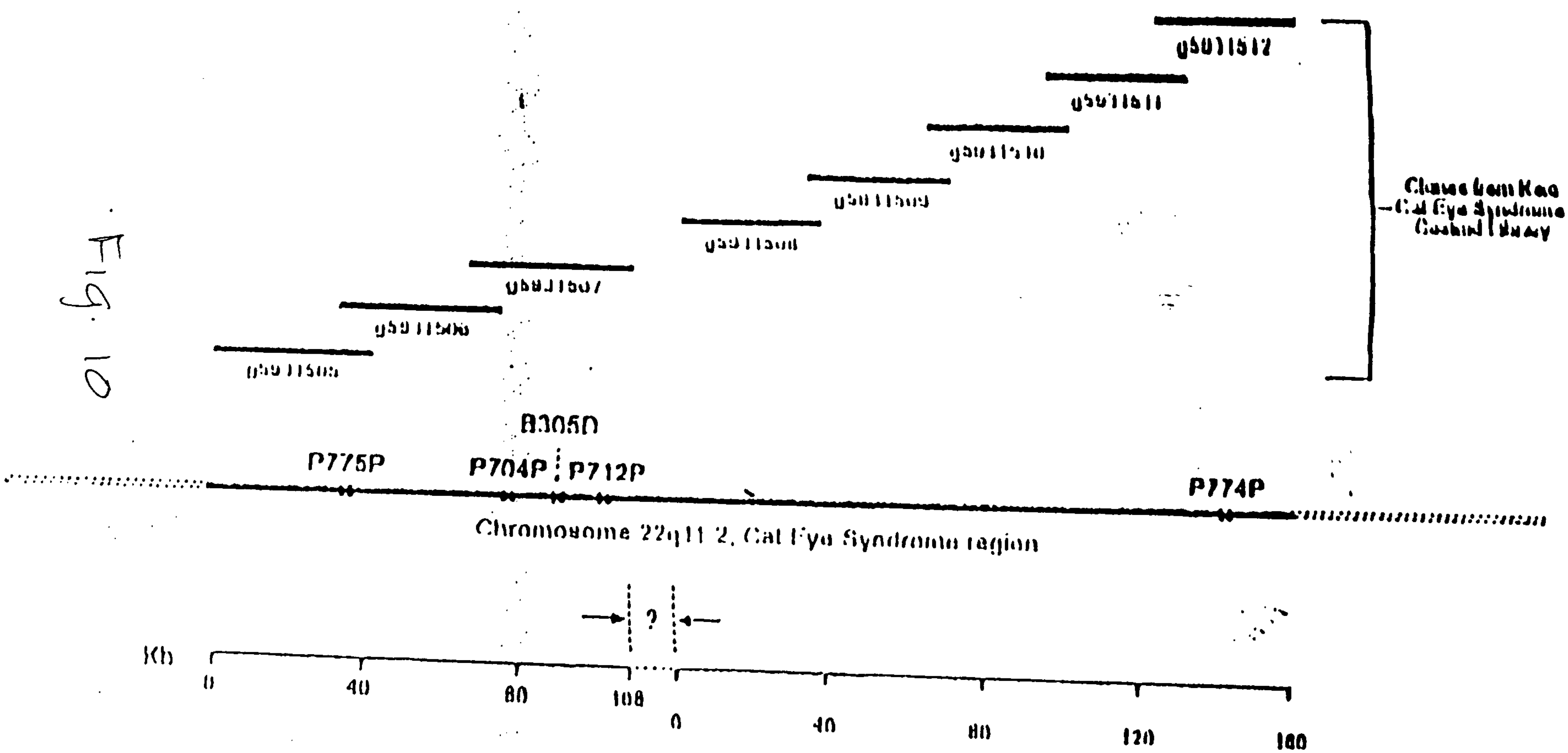


Fig. 10

FIGURE 4. Elisa assay of rabbit polyclonal antibody specificity

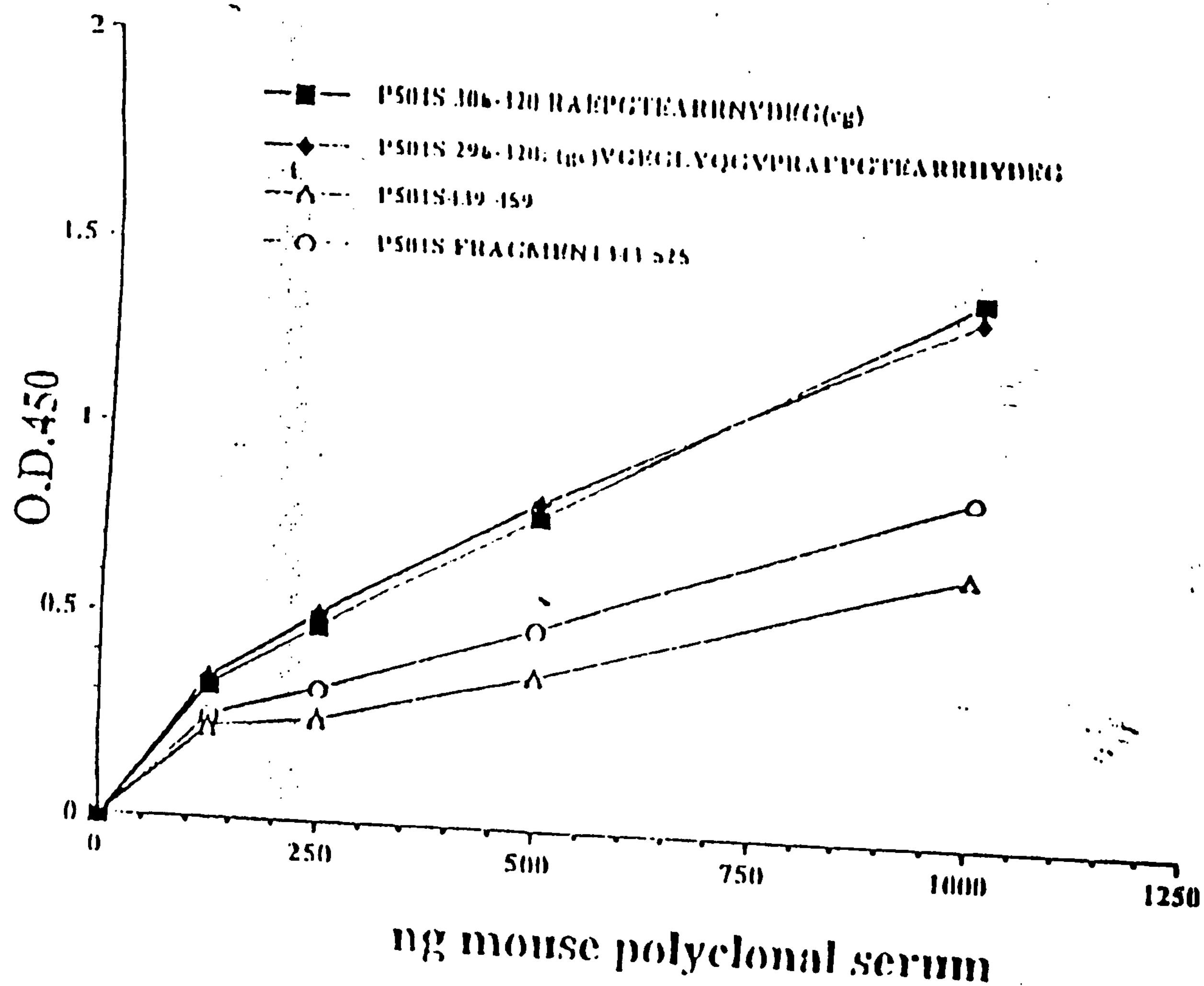


Fig. 11

10 20 30 40 50 60 70

```
GTCACTTAGGAAAAGGTGTCCTTTCGGGCAGCCGGGCTCAGCATGAGGAACAGAAGGAATGACACTCTGG 70
ACAGCACCCGGACCCTGTACTCCAGCGCGTCTCGGAGCACAGACTTGTCTTACACTGAAAGCGACTTGGT 140
GAATTTTATTCAAGCAAATTTTAAGAAACGAGAATGTGTCTTCTTTACCAAAGATTCCAAGGCCACGGAG 210
AATGTGTGCAAGTGTGGCTATGCCCAGAGCCAGCACATGGAAGGCACCCAGATCAACCAAAGTGAGAAAT 280
GGAACTACAAGAAACACACCAAGGAATTTCCTACCGACGCCTTTGGGGATATTCAGTTTGAGACACTGGG 350
```

360 370 380 390 400 410 420

```
GAAGAAAGGGAAGTATATACGTCTGTCCTGCGACACGGACGCGGAAATCCTTTACGAGCTGCTGACCCAG 420
CACTGGCACCTGAAAACACCCAACCTGGTCATTTCTGTGACCGGGGGCGCCAAGAACTTCGCCCTGAAGC 490
CGCGCATGCGCAAGATCTTCAGCCGGCTCATCTACATCGCGCAGTCCAAAGGTGCTTGGATTCTCACGGG 560
AGGCACCCATTATGGCCTGACGAAGTACATCGGGGAGGTGGTGAGAGATAACACCATCAGCAGGAGTTCA 630
GAGGAGAATATTGTGGCCATTGGCATAGCAGCTTGGGGCATGGTCTCCAACCGGGACACCCTCATCAGGA 700
```

710 720 730 740 750 760 770

```
ATTGCGATGCTGAGGGCTATTTTTTAGCCCAGTACCTTATGGATGACTTCACAAGGGATCCACTGTATAT 770
CCTGGACAACAACCACACACATTTGCTGCTCGTGGACAATGGCTGTCATGGACATCCCACTGTCGAAGCA 840
AAGCTCCGGAATCAGCTAGAGAAGCATATCTCTGAGCGCACTATTCAAGATTCCAACTATGGTGGCAAGA 910
TCCCCATTGTGTGTTTTGCCCAAGGAGGTGGAAAAGAGACTTTGAAAGCCATCAATACCTCCATCAAAAA 980
TAAAATTCCTTGTGTGGTGGTGGAAGGCTCGGGCCGGATCGCTGATGTGATCGCTAGCCTGGTGGAGGTG 1050
```

1060 1070 1080 1090 1100 1110 1120

```
GAGGATGCCCCGACATCTTCTGCCGTCAAGGAGAAGCTGGTGCGCTTTTTACCCCGCACGGTGTCCCGGC 1120
TGTCTGAGGAGGAGACTGAGAGTTGGATCAAATGGCTCAAAGAAATTCTCGAATGTTCTCACCTATTAAC 1190
AGTTATTAAAATGGAAGAAGCTGGGGATGAAATTGTGAGCAATGCCATCTCCTACGCTCTATACAAAGCC 1260
TTCAGCACCAGTGAGCAAGACAAGGATAACTGGAATGGGC-GCTGAAGCTTCTGCTGGAGTGGAACCAGC 1330
TGGACTTAGCCAATGATGAGATTTTCACCAATGACCGCCGATGGGAGTCTGCTGACCTTCAAGAAGTCAT 1400
```

1410 1420 1430 1440 1450 1460 1470

```
GTTTACGGCTCTCATAAAGGACAGACCCAAGTTTGTCCGCCTCTTTCTGGAGAATGGCTTGAACCTACGG 1470
AAGTTTCTCACCCATGATGTCCTCACTGAACTCTTCTCCAACCACTTCAGCACGCTTGTGTACCGGAATC 1540
TGCAGATCGCCAAGAATTCCTATAATGATGCCCTCCTCACGTTTGTCTGGAAACTGGTTGCGAACTTCCG 1610
AAGAGGCTTCCGGAAGGAAGACAGAAATGGCCGGGACGAGATGGACATAGAACTCCACGACGTGTCTCCT 1680
ATTACTCGGCACCCCCTGCAAGCTCTCTTCATCTGGGCCATTCTTCAGAATAAGAAGGAACTCTCCAAAG 1750
```

1760 1770 1780 1790 1800 1810 1820

```
TCATTTGGGAGCAGACCAGGGGCTGCACTCTGGCAGCCCTGGGAGCCAGCAAGCTTCTGAAGACTCTGGC 1820
CAAAGTGAAGAACGACATCAATGCTGCTGGGGAGTCCGAGGAGCTGGCTAATGAGTACGAGACCCGGGCT 1890
GTTGAGCTGTTCACTGAGTGTTACAGCAGCGATGAAGACTTGGCAGAACAGCTGCTGGTCTATTCCTGTG 1960
AAGCTTGGGGTGGAAGCAACTGTCTGGAGCTGGCGGTGGAGGCCACAGACCAGCATTTCATCGCCCAGCC 2030
TGGGGTCCAGAATTTTCTTTCTAAGCAATGGTATGGAGAGATTTCCCGAGACACCAAGAACTGGAAGATT 2100
```

Fig. 12A (1)

2110 2120 2130 2140 2150 2160 2170

TCCTGTGTCTGTTTATTATACCCTTGGTGGGCTGTGGCTTTGTATCATTTAGGAAGAAACCTGTCGACA 2170
AGCACAAGAAGCTGCTTTGGTACTATGTGGCGTTCTTCACCTCCCCCTTCGTGGTCTTCTCCTGGAATGT 2240
GGTCTTCTACATCGCCTTCCTCCTGCTGTTTGCCTACGTGCTGCTCATGGATTTCCATTCGGTGCCACAC 2310
CCCCCCGAGCTGCTCCTCTACTCCCTGGTCTTTGTCCTCTTCTGTGATGAACTCAGACAGTGGTACGTAA 2380
ATGGGGTGAATTATTTTACTGACCTGTGGAATGTGATGGACACGCTGGGGCTTTTTTACTTCATAGCAGG 2450

2460 2470 2480 2490 2500 2510 2520

AATTGTATTTCGGCTCCACTCTTCTAATAAAAGCTCTTTGTATTCTGGACGAGTCATTTTCTGTCTGGAC 2520
TACATTATTTTCACTCTAAGATTGATCCACATTTTTACTGTAAGCAGAAACTTAGGACCCAAGATTATAA 2590
TGCTGCAGAGGATGCTGATCGATGTGTTCTTCTTCCTGTTCCTCTTTGCGGTGTGGATGGTGGCCTTTGG 2660
CGTGGCCAGGCAAGGGATCCTTAGGCAGAATGAGCAGCGCTGGAGGTGGATATTCCGTTCGGTCATCTAC 2730
GAGCCCTACCTGGCCATGTTCGGCCAGGTGCCCAGTGACGTGGATGGTACCACGTATGACTTTGCCCACT 2800

2810 2820 2830 2840 2850 2860 2870

GCACCTTCACTGGGAATGAGTCCAAGCCATTGTGTGTGGAGCTGGATGAGCACAACCTGCCCCGGTTCCC 2870
CGAGTGGATCACCATCCCCCTGGTGTGCATCTACATGTTATCCACCAACATCCTGCTGGTCAACCTGCTG 2940
GTCGCCATGTTTGGCTACACGGTGGGCACCGTCCAGGAGAACAATGACCAGGTCTGGAAGTTCCAGAGGT 3010
ACTTCCTGGTGCAGGAGTACTGCAGCCGCCTCAATATCCCCTTCCCCTTCATCGTCTTCGCTTACTTCTA 3080
CATGGTGGTGAAGAAGTGCTTCAAGTGTTGCTGCAAGGAGAAAAACATGGAGTCTTCTGTCTGCTGTTTC 3150

3160 3170 3180 3190 3200 3210 3220

AAAAATGAAGACAATGAGACTCTGGCATGGGAGGGTGTCATGAAGGAAAACTACCTTGTCAAGATCAACA 3220
CAAAAGCCAACGACACCTCAGAGGAAATGAGGCATCGATTTAGACAACTGGATACAAAGCTTAATGATCT 3290
CAAGGGTCTTCTGAAAGAGATTGCTAATAAAATCAAATAAAACTGTATGAAACTCTAATGGAGAAAAATC 3360
TAATTATAGCAAGATCATATTAAGGAATGCTGATGAACAATTTTGCTATCGACTACTAAATGAGAGATTT 3430
TCAGACCCCTGGGTACATGGTGGATGATTTTAAATCACCTAGTGTGCTGAGACCTTGAGAATAAAGTGT 3500

3510 3520 3530 3540 3550 3560 3570

GTGATTGGTTTCATACTTGAAGACGGATATAAAGGAAGAATATTTCCTTTATGTGTTTCTCCAGAATGGT 3570
GCCTGTTTCTCTCTGTGTCTCAATGCCTGGGACTGGAGGTTGATAGTTTAAGTGTGTTCTTACCGCCTCC 3640
TTTTTCCTTTAATCTTATTTTTGATGAACACATATATAGGAGAACATCTATCCTATGAATAAGAACCTGG 3710
TCATGCTTTACTCCTGTATTGTTATTTGTTCATTTCCAATTGATTCTCTACTTTTCCCTTTTTGTATT 3780
ATGTGACTAATTAGTTGGCATATTGTTAAAAGTCTCTCAAATTAGGCCAGATTCTAAAACATGCTGCAGC 3850

3860 3870 3880 3890 3900 3910 3920

AAGAGGACCCCGCTCTGTTCAGGAAAAGTGTTTTCATTTCTCAGGATGCTTCTTACCTGTCAGAGGAGGT 3920
GACAAGGCAGTCTCTTGCTCTCTTGGACTCACCAGGCTCCTATTGAAGGAACCACCCCCATTCCTAAATA 3990
TGTGAAAAGTCGCCCAAAATGCAACCTTGAAAGGCACTACTGACTTTGTTCTTATTGGATACTCCTCTTA 4060
TTTATTATTTTTCCATTAAAAATAATAGCTGGCTATTATAGAAAATTTAGACCATACAGAGATGTAGAAA 4130
GAACATAAATTGTCCCCATTACCTTAAGGTAATCACTGCTAACAATTTCTGGATGGTTTTTCAAGTCTAT 4200

4210 4220 4230 4240 4250 4260 4270

TTTTTTTCTATGTATGTCTCAATTCTCTTTCAAATTTTACAGAATGTTATCATACTACATATATACTTT 4270
TTATGTAAGCTTTTTCACTTAGTATTTTATCAAATATGTTTTATTATATTCATAGCTTTCTTAAACATT 4340
ATATCAATAATTGCATAATAGGCAACCTCTAGCGATTACCATAATTTTGCTCATTGAAGGCTATCTCCAG 4410
TTGATCATTGGGATGAGCATCTTTGTGCATGAATCCTATTGCTGTATTTGGGAAATTTTCCAAGGTTAG 4480
ATTCCAATAAATATCTATTTATTATTAAATATTAAATATCGATTTATTATTAAAACCATTTATAAGGCT 4550

Fig. 12A(2)

```
      4560      4570      4580      4590      4600      4610      4620
TTTTCATAAATGTATAGCAAATAGGAATTATTAACTTGAGCATAAGATATGAGATACATGAACCTGAACT 4620
ATTAAAATAAAATATTATATTTAACCCTAGTTTAAGAAGAAGTCAATATGCTTATTTAAATATTATGGAT 4690
GGTGGGCAGATCACTTGAGGTCAGGAGTTCGAGACCAGCCTGGCCAACATGGCAAAACCACATCTCTACT 4760
AAAAATAAAAAAATTAGCTGGGTGTGGTGGTGCACTCCTGTAATCCCAGCTACTCAGAAGGCTGAGGTAC 4830
AAGAATTGCTGGAACCTGGGAGGCGGAGGTTGCAGTGAACCAAGATTGCACCACTGCACTCCAGCCGGGG 4900
      4910      4920      4930      4940      4950      4960      4970
TGACAGAGTGAGACTCCGACTGAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATATTATGG 4970
ATGGTGAAGGGAATGGTATAGAATTGGAGAGATTATCTTACTGAACACCTGTAGTCCCAGCTTTCTCTGG 5040
AAGTGGTGGTATTTGAGCAGGATGTGCACAAGGCAATTGAAATGCCCATAATTAGTTTCTCAGCTTTGAA 5110
TACACTATAAACTCAGTGGCTGAAGGAGGAAATTTTAGAAGGAAGCTACTAAAAGATCTAATTTGAAAAA 5180
CTACAAAAGCATTAACTAAAAAAGTTTATTTTCCTTTTGTCTGGGCAGTAGTGAAAATAACTACTCACAA 5250
      5260      5270      5280      5290      5300      5310      5320
CATTCACTATGTTTGCAAGGAATTAACACAAATAAAAGATGCCTTTTTACTTAAACGCCAAGACAGAAAA 5320
CTTGCCCAATACTGAGAAGCAACTTGCATTAGAGAGGGAACTGTTAAATGTTTTCAACCCAGTTCATCTG 5390
GTGGATGTTTTTGCAGGTTACTCTGAGAATTTTGCTTATGAAAAATCATTATTTTTAGTGTAGTTCACAA 5460
TAATGTATTGAACATACTTCTAATCAAAGGTGCTATGTCCTTGTGTATGGTACTAAATGTGTCCTGTGTA 5530
CTTTTGCACAACTGAGAATCCTGCGGCTTGGTTTAATGAGTGTGTTCATGAAATAAATAATGGAGGAATT 5600
      5610      5620      5630      5640      5650      5660      5670
GTCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 5662
```

Fig. 12A(3)

10 20 30 40 50 60 70

MRNRRNQTLQSTRTLYSSASRSTDLSY[illegible]SDLVNFIQANFKKRECVFFTKDSKATEN[illegible]CKCGYAQSQHME 70
GTQINQSEKWNYKKHTKEFPTDAFGDIQFETLGKKGKYIRLSCDTDAEILYELLTQHWHLKTPNLVISVT 140
GGAKNFALKPRMRKIFSRLIYIAQSKGAWILTGGTHYGLTKYIGEVVRDNTISRSSEENIVAIGIAAWGM 210
VSNRDTLIRNCDAEGYFLAQYLMDDFTRDPLYILDNNHTHLLLVDNGCHGHPTVEAKLRNQLEKHISERT 280
IQDSNYGGKIPIVCFAQGGGKETLKAINTSIKNKIPCVVVEGSGRIADVIASLVEVEDAPTSSAVKEKLV 350

360 370 380 390 400 410 420

RFLPRTVSRLSEEETESWIKWLKEILECSHLLTVIKMEEAGDEIVSNAISYALYKAFSTSEQDKDNWNGQ 420
LKLLLEWNQLDLANDEIFTNDRRWESADLQEVMFTALIKDRPKFVRLFLENGLNLRKFLTHDVLTELFSN 490
HFSTLVYRNLQIAKNSYNDALLTFVWKLVANFRRGFRKEDRNGRDEMDIELHDVSPITRHPLQALFIWAI 560
LQNKKELSKVIWEQTRGCTLAALGASKLLKTLAKVKNDINAAGESEELANEYETRAVELFTECYSSDEDL 630
AEQLLVYSCEAWGGSNCLELAVEATDQHFTAQPGVQNFLSKQWYGEISRDTKNWKIILCLFIIPLVGCGF 700

710 720 730 740 750 760 770

VSFRKKPVDKHKKLLWYYVAFFTSPFVVFSWNVVFYIAFLLLFAYVLLMDFHSVPHPPELVLYSLVFVLF 770
CDEVRQWYVNGVNYFTDLWNVMDTLGLFYFIAGIVFRLHSSNKSSLYSGRVIFCLDYIIFTLRLIHIFTV 840
SRNLGPKIIMLQRMLIDVFFFLFLFAVWMVAFGVARQGILRQNEQRWRWIFRSVIYEPYLAMFGQVPSDV 910
DGTTYDFAHCTFTGNESKPLCVELDEHNLPRFPEWITIPLVCIYMLSTNILLVNLLVAMFGYTVGTVQEN 980
NDQVWKFQRYFLVQEYCSRLNIPFPFIVFAYFYMVVKKCFKCCCKEKNMESSVCCFKNEDNETLAWEGVM 1050

1060 1070 1080 1090 1100 1110 1120

KENYLVKINTKANDTSEEMRHRFRQLDTKLNDLKGLLKEIANKIK. 1096

Fig. 12B